



STIC Search Report

Biotech-Chem Library

File Copy
09/09/2005

STIC Database Tracking Number: 169KXK

TO: David Lamberston
Location: REM/2B79/2C70
Art Unit: 1636
Tuesday, August 09, 2005

Case Serial Number: 09/982223

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Lamberston,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib*161303*

From: Lambertson, David
Sent: Tuesday, August 02, 2005 3:18 PM
To: Lambertson, David; STIC-Biotech/ChemLib
Subject: RE: Search Request

Sorry, I mistakenly removed the Default search request. Please search SEQ ID NO: 1 and 2 against the nucleotide databases for:

1. Default Search.
2. Interference Search.

Thanks.

-----Original Message-----

From: Lambertson, David
Sent: Tuesday, August 02, 2005 12:33 PM
To: STIC-Biotech/ChemLib
Cc: Lambertson, David
Subject: Search Request

Search Request

Examiner's Name:	David Lambertson
Examiner #:	79514
Art Unit:	1636
Room #:	02B79-Remsen
Mailbox room#:	02C70-Remsen
Phone:	(571) 272-0771
Results Format:	paper

Serial #:09/982,223

Please Search:

Nucleic Acid databases for:

SEQ ID No: 1 and 2

Including:

1. Interference Search

8/2/05
2 1/2 hr
2 1/2 hr
8/2/05
8/2/05

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 08:47:41 ; Search time 8137.61 seconds
 (without alignments)
 19369.833 Million cell updates/sec

Title: US-09-982-223A-2

Perfect score: 4141

Sequence: 1 atatggaaagaccacccactgtat.....agtctcccgaaaaagggggg 4141

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gbsa:*

9: gb_gbs2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
C 1	672.4	16.2	865	7 CK125894	CK125894 BBS182411
C 2	666.6	16.1	844	8 BZ574513	BZ574513 msb2_3706
C 3	662	16.0	811	9 ATHS17156	AJ517156 Arabidopsis
C 4	661.4	16.0	800	10 AJ281449	AJ281449 4A3A-P4D5
C 5	659.4	15.9	734	7 CO478328	CO478328 GQ0111-B7
C 6	656	15.8	700	5 BQ660293	BQ660293 HQ010N05W
C 7	654	15.8	1004	1 AJ281480	AJ281480 4A3A-P4G8
C 8	646.8	15.6	1048	7 CO552396	CO552396 ACI74_50
C 9	642.4	15.5	846	7 CV468077	CV468077 est_1_van
C 10	642	15.5	691	1 CB864071	CB864071 HH07007Y
C 11	638	15.4	700	6 CA305674	CA305674 EST000022
C 12	636	15.4	859	8 BZ574002	BZ574002 msb2_3462
C 13	630.8	15.2	1208	8 BZ577775	BZ577775 msb2_5567
C 14	626.8	15.1	966	8 BZ570738	BZ570738 msb2_1513
C 15	626.4	15.1	793	5 BP875099	BP875099 msb2_2693
C 16	624	15.1	1070	1 AJ281552	AJ281552 4A3A-P6P1
C 17	624	15.1	777	5 BP874724	BP874724 BP874724
C 18	623.8	15.1	854	8 BZ570648	BZ570648 msb2_1469
C 19	623.4	15.1	733	8 BZ048997	BZ048997 jnc52g07
C 20	623.4	15.1	1340	8 BZ572620	BZ572620 msb2_2721
C 21	623.4	15.1	1574	8 BZ572566	BZ572566 msb2_2693
C 22	621.4	15.0	1404	8 BZ572478	BZ572478 msb2_2653
C 23	621	15.0	665	6 CB873278	CB873278 HC11H05Y
C 24	620	15.0	754	8 BZ040933	BZ040933 lk428c05.

ALIGNMENTS

25	618.6	14.9	695	8 BH929757	BH929757 odi70d05.
26	618.4	14.9	658	8 BH97618	BH97618 odi60c01.
27	618.4	14.9	667	8 BH964466	BH964466 odi09e01.
28	618.4	14.9	682	8 BH930868	BH930868 odi10f11.
29	618.4	14.9	684	8 BH955957	BH955957 odi52g3.
30	618.4	14.9	687	8 BH962248	BH962248 odi98c02.
31	618.4	14.9	690	8 BH921350	BH921350 odi98b03.
32	618.4	14.9	690	8 BZ088472	BZ088472 lla99b11.
33	618.4	14.9	692	8 BH963078	BH963078 odi61h05.
34	618.4	14.9	692	8 BH972004	BH972004 odf8Ac07.
35	618.4	14.9	692	8 BH978479	BH978479 odf8g1.
36	618.4	14.9	693	8 BH980007	BH980007 odi10g07.
37	618.4	14.9	695	8 BH971144	BH971144 odf8l1a07.
38	618.4	14.9	697	8 BH934795	BH934795 odf8r79.
39	618.4	14.9	697	8 BH949519	BH949519 odf8B09.
40	618.4	14.9	697	8 BZ088379	BZ088379 lky38a11.
41	618.4	14.9	703	8 BH934948	BH934948 odf8h08.
42	618.4	14.9	703	8 BH938426	BH938426 odf67b06.
43	618.4	14.9	709	8 BH953754	BH953754 odi9c07.
44	618.4	14.9	709	8 BH974652	BH974652 odf55e08.
45	618.4	14.9	710	8 BH984254	BH984254 odf8f501.

/note="Vector: QB30NST (AF0474376); Site_1: Sali; Site_2:

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 01:28:50 ; Search time 1577.44 Seconds
(without alignment)
17016.962 Million cell updates/sec

Title: US-09-982-223a-2
Perfect score: 4141.
Sequence: 1 aatggaaaagccccccatgtaa...agtctccagaaaaagg99999 4141

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/1/pubpna/pctf_new_pub.seq/*
3: /cgn2_6/ptodata/1/pubpna/us05_pub.seq/*
4: /cgn2_6/ptodata/1/pubpna/us06_pubcomb.seq/*
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6: /cgn2_6/ptodata/1/pubpna/pctfs_pubcomb.seq/*
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15: /cgn2_6/ptodata/1/pubpna/us10_pubcomb.seq/*
16: /cgn2_6/ptodata/1/pubpna/us10_pubcomb.seq/*
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18: /cgn2_6/ptodata/1/pubpna/us10c_pubcomb.seq/*
19: /cgn2_6/ptodata/1/pubpna/us10c_pubcomb.seq/*
20: /cgn2_6/ptodata/1/pubpna/us10c_pubcomb.seq/*
21: /cgn2_6/ptodata/1/pubpna/us10c_pubcomb.seq/*
22: /cgn2_6/ptodata/1/pubpna/us10c_new_pub.seq/*
23: /cgn2_6/ptodata/1/pubpna/us11_pubcomb.seq/*
24: /cgn2_6/ptodata/1/pubpna/us11_new_pub.seq/*
25: /cgn2_6/ptodata/1/pubpna/us60_pubcomb.seq/*
26: /cgn2_6/ptodata/1/pubpna/us60_pubcomb.seq/*

RESULT 1
US-09-982-223a-2
; Sequence 2, Application US/0982223A
; Publication No. US09030175972A1
; GENERAL INFORMATION:
; APPLICANT: Daley, George Q.
; ATTORNEY OR INVENTION: Koh, Eugene Y.
; TITLE OF INVENTION: EXPRESSION VECTORS AND USES THEREOF
; FILE REFERENCE: 13086-102001
; CURRENT APPLICATION NUMBER: US/09/982,223A
; PRIORITY FILING DATE: 2001-10-18
; PRIORITY APPLICATION NUMBER: 60/241,879
; PRIORITY FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4141
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FRAGMENT:
; OTHER INFORMATION: Synthetically generated nucleic acid
US-09-982-223a-2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4141	100.0	4141	10 US-09-982-223a-2	Sequence 2, Appli
2	2131.6	51.5	5713	9 US-09-963-2068-5	Sequence 5, Appli
3	2131.6	51.5	5713	9 US-09-966-9764-1	Sequence 5, Appli
4	2131.6	51.5	5713	11 US-09-953-247A-5	Sequence 5, Appli
5	1840	44.4	5782	22 US-09-982-223a-1	Sequence 36, Appli
6	1825	44.1	6855	22 US-10-987-388-36	Sequence 35, Appli
7	1825	44.1	6851	22 US-10-987-388-35	

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match 100.0%; Score 4141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAGACCCACCTGTAGGTGGCAAGCTAGCGGCCGATAACTCTGTATAGCA 60
Db 1 ATGAAAGACCCACCTGTAGGTGGCAAGCTAGCGGCCGATAACTCTGTATAGCA 60

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 10:56:46 ; Search time 425.242 Seconds

(without alignments)
 15934.027 Million cell updates/sec

Title: US-09-982-223A-2

Perfect score: 4141

Sequence: 1 at-gaaaggcccccacctgtta.....agtctccggaaaagggggg 4141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued_Patent-NA:
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 2: /cgn2_6/podata/1/ina/5B_COMB.seq:
 3: /cgn2_6/podata/1/ina/6A_COMB.seq:
 4: /cgn2_6/podata/1/ina/6B_COMB.seq:
 5: /cgn2_6/podata/1/ina/PCTUS_COMB.seq:
 6: /cgn2_6/podata/1/ina/backfile1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
C 1	1825	44.1	10100	3	US-09-133-944-1	Sequence 1, Appli
C 2	1825	44.1	10100	3	US-09-208-027-1	Sequence 1, Appli
C 3	1825	44.1	10100	4	US-10-043-074-1	Sequence 1, Appli
C 4	1819.8	43.9	6350	2	US-08-385-135A-8	Sequence 1, Appli
C 5	1597.8	38.6	8614	3	US-09-208-027-5	Sequence 5, Appli
C 6	1597.8	38.6	8614	4	US-10-043-074-5	Sequence 5, Appli
C 7	1497.6	36.2	6620	4	US-08-786-531B-3	Sequence 3, Appli
C 8	1495	36.1	5363	4	US-08-786-531B-3	Sequence 2, Appli
C 9	1437.8	34.7	8387	2	US-08-532-814-1	Sequence 1, Appli
C 10	1437.8	34.7	8388	3	US-08-925-509-1	Sequence 1, Appli
C 11	1420.6	34.3	7617	3	US-08-646-538-34	Sequence 1, Appli
C 12	1420.6	34.3	7617	3	US-09-503-222-34	Sequence 34, Appli
C 13	1337.4	33.2	8202	1	US-08-258-420-13	Sequence 13, Appli
C 14	1230.8	29.7	6700	4	US-09-654-449-1	Sequence 1, Appli
C 15	1230.8	29.7	8175	4	US-09-759-152A-8	Sequence 8, Appli
C 16	1230.8	29.7	8175	4	US-09-654-449-4	Sequence 4, Appli
C 17	1230.8	29.7	8175	4	US-09-654-449-5	Sequence 5, Appli
C 18	1230.8	29.7	8518	4	US-09-654-449-5	Sequence 3, Appli
C 19	1229.2	29.7	6700	4	US-09-759-152A-3	Sequence 1, Appli
C 20	1229.2	29.7	8175	4	US-09-759-152A-6	Sequence 6, Appli
C 21	1229.2	29.7	8161	4	US-09-759-152A-4	Sequence 4, Appli
C 22	1196.2	28.9	8316	1	US-07-753-520B-4	Sequence 4, Appli
C 23	1196.2	28.9	9115	1	US-07-753-520B-3	Sequence 3, Appli
C 24	1194	28.8	6365	4	US-08-352-990-1	Sequence 1, Appli
C 25	1193.8	28.8	7235	4	US-08-786-531B-6	Sequence 6, Appli
C 26	1192.6	28.8	7699	4	US-09-645-004-1	Sequence 1, Appli
C 27	1192.6	28.8	7980	4	US-09-645-004-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-09-133-944-1/C
 ; Sequence 1, Application US/09133944
 ; Patent No. 6280937
 ; GENERAL INFORMATION:
 ; APPLICANT: Luo, Ying
 ; APPLICANT: Lorens, James B
 ; TITLE OF INVENTION: SHUTTLE VECTORS
 ; FILE REFERENCE: A66-552/DVB/DAV
 ; CURRENT APPLICATION NUMBER: US/09/133,944
 ; CURRENT FILING DATE: 1999-08-14
 ; EARLIER APPLICATION NUMBER: 09/133,949
 ; EARLIER FILING DATE: 1998-08-14
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 10100
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description
 ; OTHER INFORMATION: vectors
 ; OTHER INFORMATION: constructed
 ; OTHER INFORMATION: Description
 ; OTHER INFORMATION: vectors
 ; OTHER INFORMATION: constructed
 ; OTHER INFORMATION: vectors
 ; OTHER INFORMATION:保守性
 ; OTHER INFORMATION: 0; Mismatches 20; Indels 2; Gaps 2;
 ; OTHER INFORMATION: 96; CTAAGCTTAAGTCGAACTGGCCATTTGCGGCTACGGATATGGCTGTG 215
 ; OTHER INFORMATION: 96; CTAGCTTAACTGAACTGGCCATTTGCGGCTACGGATATGGCTGTG 155
 ; OTHER INFORMATION: 9382; CTAGCTTAACTGAACTGGCCATTTGCGGCTACGGATATGGCTGTG 9323
 ; OTHER INFORMATION: 156; TCTAGATAAAGTCGAACTGGCCATTTGCGGCTACGGATATGGCTGTG 215
 ; OTHER INFORMATION: 9332; TCTAGATCTAGCTCAGGACATGGCAACTGGCTATCTGGCT 9263
 ; OTHER INFORMATION: 216; GTTACGGCATTTCTGCCCGGCTAGGCCCAAGAACATGGCAACAGCTGAATATGGGCCA 275
 ; OTHER INFORMATION: 9262; GTTACGGCATTTCTGCCCGGCTAGGCCCAAGAACATGGCAACAGCTGAATATGGGCCA 9203
 ; OTHER INFORMATION: 276; AACAGGATATCTGTTGAACTGAGTTCTGCCGGCTACGGACAGATGGCTCC 335
 ; OTHER INFORMATION: 9202; AACAGGATATCTGTTGAACTGAGTTCTGCCGGCTACGGACAGATGGCTCC 9143
 ; OTHER INFORMATION: 336; CAGATGGCTCCAGGCTTCAAGAACCTCAGTTCCAGGCTGGTGCCTCC 395
 ; OTHER INFORMATION: 9142; CAGATGGCTCCAGGCTTCAAGAACCTCAGTTCCAGGCTGGTGCCTCC 9083
 ; OTHER INFORMATION: 396; AAGGACTCTGAAATGACCCCTGTGCTTATTGAACTACCATGTTGCTTC 455

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 08:47:41 ; Search time 11362.4 Seconds

(without alignments)

19369.833 Million cell updates/sec

US-09-982-223A-1

Perfect score: 5782

Sequence: 1 aatgaaagacccacctgtta.....tccgcgcacatccctgtcat 5782

Scoring table: IDENTITY_NTC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters:

68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : EST:^{*}

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1014.2	17.5	AJ2811552	AJ2811552 4A3A-P6F1
2	976.6	16.9	C0552396	C0552396 Acly4_50
c 3	943.2	16.3	B0438846	BM438846 iPLvR0015
c 4	882.4	15.3	AJ2811480	AJ2811480 4A3A-P4G8
c 5	863.8	14.9	CR753463	CR753463 DXFZp169G
c 6	854.6	14.8	BG838279	BG838279 Gc01 1.0e0
c 7	848.2	14.7	C0487414	C0487414 CO00227_B7
c 8	839.4	14.5	AL042026	AL042026 DXFZp134B
c 9	827	14.3	CP269552	CP269552 PcyICol0d8
c 10	823	14.2	B0438950	BM438950 iPLvR0049
c 11	818.8	14.2	CK125894	CK125894 BE184411
c 12	807.6	14.0	B2570738	B2570738 msh2_1513
c 13	806.8	14.0	CN823189	CN823189 oa_sp1.bn
c 14	806.4	13.9	CD649375	CD649375 CyGnd008
c 15	803.2	13.9	B2577702	B2577702 msh2_5533
c 16	793.8	13.7	B2572284	B2572284 msh2_2572
c 17	791.4	13.7	CN823902	CN823902 oa_sp1.bn
c 18	789.4	13.7	B2576726	B2576726 msh2_5071
c 19	779.8	13.5	CV468077	CV468077 est_1 van
c 20	775.4	13.4	CR753457	CR753457 DXFZp169P
c 21	773.8	13.4	AU081137	AU081137
c 22	773.4	13.4	AL044364	AL044364 DKF29434C
c 23	773.2	13.4	B2575810	B2575810 msh2_4637
c 24	772.8	13.4	CD280920	CD280920 G44224_42

ALIGNMENTS

c 25	769.8	13.3	CN8224433	Oa_sp1.bn
c 26	764.2	13.2	CV224987	CS hyp_24
c 27	761.6	13.2	B0825653	1030129610
c 28	758.4	13.1	B2572566	msh2_2893
c 29	755.4	13.1	CD279661	G3818_35
c 30	753.8	13.0	B2571475	msh2_1906
c 31	752	13.0	B2571721	msh2_2005
c 32	749.8	13.0	CN823164	Oa_sp1.bn
c 33	747.4	12.9	CR766850	DXFZp48H
c 34	745.4	12.9	B2574513	msh2_3706
c 35	743.8	12.9	AU281449	4A3A-P4D5
c 36	742.4	12.8	AU081124	AU081124
c 37	740.6	12.8	CE752100	TGDR9_Hum
c 38	739.4	12.8	CD281097	GI4221_74
c 39	739.2	12.8	B2569398	PAC82-164
c 40	733.2	12.7	ATH517156	AJ517156
c 41	732.2	12.7	B2571229	msh2_1741
c 42	728.4	12.6	CD281097	GI4224_38
c 43	728.4	12.6	CO477685	GQ0132_B7
c 44	728.2	12.6	B2576702	msh2_5060
c 45	727.6	12.6	CK122661	BBSJ382410

RESULT 1				
LOCUS	DEFINITION	VERSION	KEYWORDS	ORGANISM
AJ2811552	4A3A-P6F1-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P6F11, mRNA sequence.	AU2811552	EST	Anopheles gambiae (African malaria mosquito)
		AU2811552.1	GI:69294322	Anopheles gambiae
			1 (bases 1 to 1070)	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
			REFERENCE AUTHORS	Dimopoulos, G., Cabavant, T.L., Chang, S., Scheets, T., Roberts, C., Donohus, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Katatos, F.C.
			TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
			JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
			MEDLINE	20300950
			PUBMED	10841561
			COMMENT	Contact: Dimopoulos, G. European Molecular Biology Laboratory Meyerhofstrasse 1, 6911 Heidelberg, Germany.
				Location/Qualifiers
				1..1070
			/organism="Anopheles gambiae" /mol_type="mRNA" /strain="4A_r/r" /db_xref="taxon:7165" /clone="4A3A-P6F11" /cell_line="immune competent 4A3A" /lab_host="E. coli DH10B" /clone_lib="Anopheles gambiae immune competent 4A3A" /notes="vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."	

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2005, 02:13:00 ; Search time 1851.78 Seconds

(without alignments)
18483.824 Million cell updates/sec

Title: US-09-982-223A-1

Perfect score: 5782

Sequence: 1 aatggaaaagccaccactgtat.....tccggcacatttcgtcat 5782

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$

Maximum Match 100\$

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s;*

2: geneseqn1990s;*

3: geneseqn2000s;*

4: geneseqn2001as;*

5: geneseqn2001bs;*

6: geneseqn2002as;*

7: geneseqn2002bs;*

8: geneseqn2003as;*

9: geneseqn2003bs;*

10: geneseqn2003cs;*

11: geneseqn2003ds;*

12: geneseqn2004as;*

13: geneseqn2004bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	5782	100.0	5782	6 ABC85887	Abk85887 DNA sequence
2	3657.2	63.3	6221	3 AA234935	Aaf30944 Vector us
3	3657.2	63.3	6221	4 AAF30944	Adq80674 Bcl-XL ex
4	3500.6	61.9	5903	13 ADQ80674	Aaz34936 Retrovirus
5	3334.6	57.7	5715	3 AA234936	Aaf30945 Vector us
6	3334.6	57.7	5715	4 AAF30945	Abx13168 Retrovira
7	3213	55.6	7654	8 ABX13168	Adq80673 Bcl-XL ex
8	3213	55.6	7654	10 ADQ80673	Aai67595 Nucleotid
9	3118.6	53.9	6444	6 AA167595	Aav83182 Intermedi
10	3118	53.9	6444	2 AA167595	Aaf85611 M-MuLV-ba
11	3116.2	53.9	6145	5 AAF85611	Aax90481 Plasmid r
12	3116.2	53.9	6145	2 AAX90481	Aax90482 Plasmid r
13	3085	53.4	6141	8 AAX90482	Aax90483 Plasmid r
14	3066.2	53.0	6522	2 AAX90482	Aag41173 Plasmid L
15	3023	52.3	6365	2 AAO41173	Adg82626 Clone plx
16	2959.8	51.9	6046	12 ADG82626	Ade82653 Plasmid v
17	2911.4	51.7	6620	6 ADE82653	Aax33181 Base sequ
18	2906	51.6	6544	4 AAX33181	Ada12887 Murine le
19	2909.6	51.4	6620	9 ADA12887	Aax90484 Plasmid r
20	2871.6	49.7	5874	2 AAX90484	

ALIGNMENTS

RESULT 1
ID ABK85887 standard: DNA: 5782 BP.
XX
AC ABK85887;
XX
DT 21-AUG-2002 (first entry)
XX
DE DNA sequence encoding Gag packaging protein.
XX
DE DNA sequence encoding Gag packaging protein.
XX
OS Unidentified.
XX
PN WO200234929-A2.
XX
PD 02-MAY-2002.
XX
PP 18-OCT-2001; 2001WO-US032592.
XX
PR 20-OCT-2000; 2000US-0241879P.
XX
PR 02-MAY-2002.

(WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PA PA
XX
PI Kohn BY, Daley GQ;
XX
DR WPI: 2002-489949/P.
XX
PT Expression vectors comprising viral vectors (e.g. retroviral vectors), useful for generating or screening nucleic acid libraries or in antisense based or gene trapping methods for identifying modulators of a mammalian gene.
XX
PT Claim 8; Fig 1; 11pp; English.
XX
CC This invention relates to a novel vector comprising from 5' to 3', a packaging sequence, heterologous insert sequence or restriction site for insertion of a heterologous sequence and a 3' long terminal repeat (LTR) sequence, where at least 2 codons of the packaging sequence are altered to reduce formation of fusion polypeptides encoded by the packaging sequence or a portion of it, and the heterologous insert sequence. The vector of the invention is useful for generating a library and in screening nucleic acid libraries. In particular, the vector is

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MCCM numerical - multiscale search - unstructured model

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Run on: August 8, 2005, 02:23:00 ; Search time 16026.8 Seconds
without alignment) 17481 226 Million cell windows/proc

Title: US-09-982-223A-1
Barcode: 22000000000000000000000000000000

Percent score: 3/82 Sequence: 1 aatggaaagaccccacctgtatccccc

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

post-processing: Minimum Match 0% Maximum Match 100% Fixer 45 minutes

Database : GenEmbl : Structuring lists in summaries

1: gb_ba: *
2: gb_htg: *
3: cb_in: *

4. "gb-om: *
5. "gb-ov: *

6: 9b-pac:*

9: g_b_pr:*

10: g_b_ro:*

11: g_b_arcs:*

12: gb_SY:*
13: gb_un:*

Pred. No. is the number of results predicted by

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID
	1	5782	100.0	5782	6	AX91314	
	2	3948	68.3	5983	12	AB041927	
	3	3922.4	67.8	6076	12	AB086386	
	4	3897.2	67.4	6148	12	AB041928	
	5	3820.8	65.8	5304	12	AB086384	
	6	3802	65.8	5901	12	AB086388	
	7	3794.2	65.6	6277	12	AB086385	
	8	3786.2	65.5	6101	12	AP132211	
	9	3633.4	62.8	6119	6	BD222120	
	10	3633.4	62.8	6219	6	AK146810	
	11	3580.6	61.9	5903	6	CQ079092	
	12	3389.2	58.6	6690	12	AB086389	
	13	3310.6	57.3	5713	6	BD22121	
	14	3310.6	57.3	5713	6	AX146811	
	15	3279.2	56.7	6624	12	AB086387	
	16	3174.4	54.9	6374	12	SNTMNOV1	
	17	3163.8	54.7	6259	12	SNTMNRV	
	18	3119.4	54.0	6149	12	SNTMMPLN2	
	19	3118.6	53.9	7257	6	CQ079091	

AR140313	Sequence 1
I77211	Sequence 1
BR53338	Sequence 1
BD105951	Animal m
M66553	Moloney m
BD138562	Expressai
BD138563	Expressai
U00220	Human imm
AF113968	Cloning
BD8622	Bicistronic
I70974	Sequence 1
AR302094	Sequence
E23356	Virus vect
AXB23828	Sequence
M28547	Retrovirra
AR164477	Sequence
BD138565	Expressai
M28248	Retrovirra
AX14854	Sequence
AF132210	Cloning
M6754	Moloney m
AX133941	Sequence
AXB23827	Sequence
BD269812	Retrovir
AX004549	Sequence
AX004569	Sequence

ALIGNMENTS

RESULT 1
AX491314 AX491314 LOCUS AX491314 DEFINITION Sequence 1 from Patent WO0234929.
ACCESSION AX491314 ACCESSION AX491314
VERSION AX491314.1 VERSION AX491314.1 GI:22324009
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences
AUTHORS Kohn, B.Y. and Daley, G.Q.
TITLE Expression vectors and uses thereof
JOURNAL Patent: WO 0234929-A-1 02-MAY-2002;
FEATURES WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
LOCATION/QUALIFIERS Location/Qualifiers
 1. 5782 /organism="synthetic construct"
 /mol type="unassigned DNA"
 /db Xref="taxon:32630"
 /note="Synthetically generated nucleic acid"

100.0% ; Score 5782 ; DB 6 ; Length 5782

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0

Qy	1	AATGAAGACCCACCTGTAGGTTGGCAAGCTTAACTGAAACCCATTGCAAGGC	60
Db	1	AATGAAGACCCACCTGTAGGTTGGCAAGCTTAACTGAAACCCATTGCAAGGC	60
Qy	61	ATGGAAAATACATACATGAAATAGAAAAGTTCAAGTCAAGTCAAGGTCAAGG	120
Db	61	ATGGAAAATACATACATGAAATAGAAAAGTTCAAGTCAAGTCAAGGTCAAGG	120
Qy	121	AGCTGAATAATGGCCAAGGGATAATCTGTGTTAACAGTTCCTGCCGGTCAGGGCC	180
Db	121	AGCTGAATAATGGCCAAGGGATAATCTGTGTTAACAGTTCCTGCCGGTCAGGGCC	180
Qy	181	AAGAACGATGGAACGCGTAATGGCCAAACAGGATATCTGTGTTAACAGTTCCTG	240
Db	181	AAGAACGATGGAACGCGTAATGGCCAAACAGGATATCTGTGTTAACAGTTCCTG	240